

Serial Number: 09/938,901**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file.
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form

2/1/95

RAW SEQUENCE LISTING

DATE: 10/16/2001

PATENT APPLICATION: US/09/938,901

TIME: 17:37:13

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10162001\I938901.raw

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3 <110> APPLICANT: Kuramitsu Seiki,
4     Yokoyama Shigeyuki
6 <120> TITLE OF INVENTION: GENE ENCODING DNA REPAIR ENZYME
8 <130> FILE REFERENCE: PH-1261-US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/938,901
C--> 11 <141> CURRENT FILING DATE: 2001-08-24
13 <150> PRIOR APPLICATION NUMBER: JP2001-47762
14 <151> PRIOR FILING DATE: 2001-02-23
16 <160> NUMBER OF SEQ ID NOS: 17
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 975
22 <212> TYPE: DNA
23 <213> ORGANISM: Thermus thermophilus
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(975)
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34 cgc ccc ctc ccc tgg cgg ggg gag aag gac cct tac cgc gtc ctg gtc      96
35 Arg Pro Leu Pro Trp Arg Gly Glu Lys Asp Pro Tyr Arg Val Leu Val
36      20      25      30
38 tcc gag gtc ctt ctg cag cag acc cgg gtg gag cag gcc ctc ccc tat      144
39 Ser Glu Val Leu Leu Gln Gln Thr Arg Val Glu Gln Ala Leu Pro Tyr
40      35      40      45
42 tac cgc cgc ttt ctg gag cgc ttt ccc acc ctg aag gcc ctg gcc gcg      192
43 Tyr Arg Arg Phe Leu Glu Arg Phe Pro Thr Leu Lys Ala Leu Ala Ala
44      50      55      60
46 gct tcc ctg gaa gag gtc ctt agg gtc tgg cag ggg gcg ggc tac tac      240
47 Ala Ser Leu Glu Glu Val Leu Arg Val Trp Gln Gly Ala Gly Tyr Tyr
48 65      70      75      80
50 cgg cgg gcg gaa cac ctc cac cgc ctg gcc cga agc gtg gag gag ctt      288
51 Arg Arg Ala Glu His Leu His Arg Leu Ala Arg Ser Val Glu Glu Leu
52      85      90      95
54 ccc ccg agc ttc gcc gag ctt cgg ggg ctt cct ggt ctc ggg cct tac      336
55 Pro Pro Ser Phe Ala Glu Leu Arg Gly Leu Pro Gly Leu Gly Pro Tyr
56      100      105      110
58 acc gcg gcg gcg gtg gcc tcc atc gcc ttc ggg gag cgg gtg gcg gcg      384
59 Thr Ala Ala Ala Val Ala Ser Ile Ala Phe Gly Glu Arg Val Ala Ala
60      115      120      125
62 gtg gac ggg aac gtc cgg agg gtc ctc tcc cgc ctc ttc gcc cgg gaa      432
63 Val Asp Gly Asn Val Arg Arg Val Leu Ser Arg Leu Phe Ala Arg Glu
64      130      135      140
66 agc ccc aag gag aag gag ctt ttc gcc ctc gcc cag ggc ctc ctc ccc      480
67 Ser Pro Lys Glu Lys Glu Leu Phe Ala Leu Ala Gln Gly Leu Leu Pro

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68 145          150          155          160
70 gag ggc gtg gac ccg ggg gtg tgg aac cag gcc ctc atg gag ctc ggg 528
71 Glu Gly Val Asp Pro Gly Val Trp Asn Gln Ala Leu Met Glu Leu Gly
72          165          170          175
74 gcc acg gtc tgc ctg ccg aaa cgg ccc cgt tgc ggg gcc tgc ccc cta 576
75 Ala Thr Val Cys Leu Pro Lys Arg Pro Arg Cys Gly Ala Cys Pro Leu
76          180          185          190
78 ggg gcc ttc tgc cgg ggg aag gag gcc ccc ggg cgc tac ccc gcg ccc 624
79 Gly Ala Phe Cys Arg Gly Lys Glu Ala Pro Gly Arg Tyr Pro Ala Pro
80          195          200          205
82 agg aag cgc cgg gcg aag gag gag cgc ctc gtc gcc ctc gtc ctc ctc 672
83 Arg Lys Arg Arg Ala Lys Glu Glu Arg Leu Val Ala Leu Val Leu Leu
84          210          215          220
86 ggg cgg aag ggg gtg cac ctg gaa agg ctt gag ggg cgc ttc cag ggc 720
87 Gly Arg Lys Gly Val His Leu Glu Arg Leu Glu Gly Arg Phe Gln Gly
88 225          230          235          240
90 ctc tac ggc gtc ccc ctc ttt ccc cct gag gag ctt ccc ggg cgg gag 768
91 Leu Tyr Gly Val Pro Leu Phe Pro Pro Glu Glu Leu Pro Gly Arg Glu
92          245          250          255
94 gcg gcc ttc ggg gtg agg tct agg ccc cta gcc gag gtg cgc cac gcc 816
95 Ala Ala Phe Gly Val Arg Ser Arg Pro Leu Gly Glu Val Arg His Ala
96          260          265          270
98 ctc acc cac cgg agg ctt cgc gtg gag gtg cgg ggg gcc ctt tgg gaa 864
99 Leu Thr His Arg Arg Leu Arg Val Glu Val Arg Gly Ala Leu Trp Glu
100          275          280          285
102 ggg gag ggg gag gac ccc tgg aag agg ccc cta ccc aag ctc atg gag 912
103 Gly Glu Gly Glu Asp Pro Trp Lys Arg Pro Leu Pro Lys Leu Met Glu
104          290          295          300
106 aag gtg ctc cgc aag gcg ctt ccc ctc ctc gct cat gcg gcc gta gtc 960
107 Lys Val Leu Arg Lys Ala Leu Pro Leu Leu Ala His Ala Gly Val Val
108 305          310          315          320
110 ccc ctc ccg gac gca 975
111 Pro Leu Pro Asp Ala
112          325
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116 <211> LENGTH: 325
117 <212> TYPE: PRT
118 <213> ORGANISM: Thermus thermophilus
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125          20          25          30
127 Ser Glu Val Leu Leu Gln Gln Thr Arg Val Glu Gln Ala Leu Pro Tyr
128          35          40          45
130 Tyr Arg Arg Phe Leu Glu Arg Phe Pro Thr Leu Lys Ala Leu Ala Ala
131          50          55          60
133 Ala Ser Leu Glu Glu Val Leu Arg Val Trp Gln Gly Ala Gly Tyr Tyr
134 65          70          75          80

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137                85                90                95
139 Pro Pro Ser Phe Ala Glu Leu Arg Gly Leu Pro Gly Leu Gly Pro Tyr
140                100                105                110
142 Thr Ala Ala Val Ala Ser Ile Ala Phe Gly Glu Arg Val Ala Ala
143                115                120                125
145 Val Asp Gly Asn Val Arg Arg Val Leu Ser Arg Leu Phe Ala Arg Glu
146                130                135                140
148 Ser Pro Lys Glu Lys Glu Leu Phe Ala Leu Ala Gln Gly Leu Leu Pro
149 145                150                155                160
151 Glu Gly Val Asp Pro Gly Val Trp Asn Gln Ala Leu Met Glu Leu Gly
152                165                170                175
154 Ala Thr Val Cys Leu Pro Lys Arg Pro Arg Cys Gly Ala Cys Pro Leu
155                180                185                190
157 Gly Ala Phe Cys Arg Gly Lys Glu Ala Pro Gly Arg Tyr Pro Ala Pro
158                195                200                205
160 Arg Lys Arg Arg Ala Lys Glu Glu Arg Leu Val Ala Leu Val Leu Leu
161                210                215                220
163 Gly Arg Lys Gly Val His Leu Glu Arg Leu Glu Gly Arg Phe Gln Gly
164 225                230                235                240
166 Leu Tyr Gly Val Pro Leu Phe Pro Pro Glu Glu Leu Pro Gly Arg Glu
167                245                250                255
169 Ala Ala Phe Gly Val Arg Ser Arg Pro Leu Gly Glu Val Arg His Ala
170                260                265                270
172 Leu Thr His Arg Arg Leu Arg Val Glu Val Arg Gly Ala Leu Trp Glu
173                275                280                285
175 Gly Glu Gly Glu Asp Pro Trp Lys Arg Pro Leu Pro Lys Leu Met Glu
176                290                295                300
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186 <211> LENGTH: 1998
187 <212> TYPE: DNA
188 <213> ORGANISM: Thermus thermophilus
190 <220> FEATURE:
191 <221> NAME/KEY: CDS
192 <222> LOCATION: (1)..(1998)
194 <400> SEQUENCE: 3
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196 Met Arg Asp Arg Val Arg Trp Arg Val Leu Ser Leu Pro Pro Leu Ala
197 1 5 10 15
199 cag tgg cgg gag gtg atg gcg gcc ttg gag gtg ggg ccg gag gcc gcc 96
200 Gln Trp Arg Glu Val Met Ala Ala Leu Glu Val Gly Pro Glu Ala Ala
201 20 25 30
203 ctg gcc tac tgg cac cgg ggc ttt agg cgc aag gag gac ctg gac ccc 144
204 Leu Ala Tyr Trp His Arg Gly Phe Arg Arg Lys Glu Asp Leu Asp Pro
205 35 40 45

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208	Pro	Leu	Ala	Leu	Leu	Pro	Leu	Lys	Gly	Leu	Arg	Glu	Ala	Ala	Ala	Leu	
209		50					55					60					
211	ctg	gag	gag	gcg	ctc	cgc	cag	ggg	aag	cgg	atc	cgc	gtc	cac	ggg	gac	240
212	Leu	Glu	Glu	Ala	Leu	Arg	Gln	Gly	Lys	Arg	Ile	Arg	Val	His	Gly	Asp	
213	65					70				75						80	
215	tac	gac	gcc	gac	ggg	ctc	acg	ggc	acg	gcc	atc	ctg	gtt	cgg	ggc	ctc	288
216	Tyr	Asp	Ala	Asp	Gly	Leu	Thr	Gly	Thr	Ala	Ile	Leu	Val	Arg	Gly	Leu	
217					85					90					95		
219	gcc	gcc	ttg	ggc	gcc	gac	gtc	cac	ccc	ttc	atc	ccc	cac	cgg	ctg	gag	336
220	Ala	Ala	Leu	Gly	Ala	Asp	Val	His	Pro	Phe	Ile	Pro	His	Arg	Leu	Glu	
221				100					105					110			
223	gaa	ggg	tac	ggg	gtg	ctg	atg	gag	cgg	gtt	ccc	gag	cac	ctc	gag	gcc	384
224	Glu	Gly	Tyr	Gly	Val	Leu	Met	Glu	Arg	Val	Pro	Glu	His	Leu	Glu	Ala	
225			115					120					125				
227	tcg	gac	ctc	ttc	ctc	acc	gtg	gac	tgc	ggg	atc	acg	aac	cac	gcc	gag	432
228	Ser	Asp	Leu	Phe	Leu	Thr	Val	Asp	Cys	Gly	Ile	Thr	Asn	His	Ala	Glu	
229			130					135					140				
231	ctc	agg	gag	ctt	ttg	gaa	aac	ggg	gtg	gag	gtg	atc	gtc	acc	gac	cac	480
232	Leu	Arg	Glu	Leu	Leu	Glu	Asn	Gly	Val	Glu	Val	Ile	Val	Thr	Asp	His	
233	145					150					155					160	
235	cac	acc	ccc	ggc	aag	acc	cct	tcc	ccc	ggc	ctc	gtg	gtc	cac	ccc	gcc	528
236	His	Thr	Pro	Gly	Lys	Thr	Pro	Ser	Pro	Gly	Leu	Val	Val	His	Pro	Ala	
237					165					170						175	
239	ctc	acc	ccg	gac	ctt	aag	gag	aag	ccc	acg	ggg	gcg	ggg	gtg	gtc	ttc	576
240	Leu	Thr	Pro	Asp	Leu	Lys	Glu	Lys	Pro	Thr	Gly	Ala	Gly	Val	Val	Phe	
241				180					185					190			
243	ctc	ctc	ctc	tgg	gcc	ctc	cac	gag	cgc	ctg	ggc	ctt	ccc	cca	ccc	ctg	624
244	Leu	Leu	Leu	Trp	Ala	Leu	His	Glu	Arg	Leu	Gly	Leu	Pro	Pro	Pro	Leu	
245			195					200					205				
247	gag	tac	gcc	gac	ctc	gcc	gcg	gtg	ggc	acc	atc	gcc	gac	gtg	gcc	ccc	672
248	Glu	Tyr	Ala	Asp	Leu	Ala	Ala	Val	Gly	Thr	Ile	Ala	Asp	Val	Ala	Pro	
249			210					215					220				
251	ctt	tgg	ggc	tgg	aac	cgg	gcc	ttg	gtg	aag	gag	ggc	ctg	gcc	cgc	atc	720
252	Leu	Trp	Gly	Trp	Asn	Arg	Ala	Leu	Val	Lys	Glu	Gly	Leu	Ala	Arg	Ile	
253	225					230					235					240	
255	ccc	gcc	tcc	tcc	tgg	gtt	ggg	ctc	agg	ctt	ctg	gcc	gag	gcg	gtg	ggg	768
256	Pro	Ala	Ser	Ser	Trp	Val	Gly	Leu	Arg	Leu	Leu	Ala	Glu	Ala	Val	Gly	
257					245					250					255		
259	tac	acg	ggg	aag	gcg	gtg	gag	gtg	gcc	ttc	cgc	atc	gcc	ccc	cgg	atc	816
260	Tyr	Thr	Gly	Lys	Ala	Val	Glu	Val	Ala	Phe	Arg	Ile	Ala	Pro	Arg	Ile	
261				260					265						270		
263	aac	gcg	gca	agc	cgc	ctc	ggg	gag	gct	gag	aag	gcc	cta	agg	ctc	ctc	864
264	Asn	Ala	Ala	Ser	Arg	Leu	Gly	Glu	Ala	Glu	Lys	Ala	Leu	Arg	Leu	Leu	
265			275					280					285				
267	ctc	acc	gac	gac	gcg	gcc	gag	gcc	cag	gcc	ctc	gtg	ggg	gaa	ctc	cac	912
268	Leu	Thr	Asp	Asp	Ala	Ala	Glu	Ala	Gln	Ala	Leu	Val	Gly	Glu	Leu	His	
269			290					295					300				
271	cgg	ctg	aac	gcc	cgc	cgc	cag	acc	ctg	gag	gag	gcc	atg	ctc	agg	aag	960

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272	Arg	Leu	Asn	Ala	Arg	Arg	Gln	Thr	Leu	Glu	Glu	Ala	Met	Leu	Arg	Lys	
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275	ctc	ctc	ccc	cag	gcg	gac	ccc	gag	gcc	aag	gcc	atc	gtc	ctc	ctg	gac	1008
276	Leu	Leu	Pro	Gln	Ala	Asp	Pro	Glu	Ala	Lys	Ala	Ile	Val	Leu	Leu	Asp	
277				325						330					335		
279	ccc	gag	ggg	cac	ccg	ggg	gtg	atg	ggc	atc	gtg	gcg	agc	cgc	atc	ctg	1056
280	Pro	Glu	Gly	His	Pro	Gly	Val	Met	Gly	Ile	Val	Ala	Ser	Arg	Ile	Leu	
281				340					345					350			
283	gag	gcc	acc	ctc	cgg	ccc	gtc	ttc	ctg	gtg	gcc	cag	ggc	aag	ggg	acg	1104
284	Glu	Ala	Thr	Leu	Arg	Pro	Val	Phe	Leu	Val	Ala	Gln	Gly	Lys	Gly	Thr	
285			355					360					365				
287	gtg	cgg	agc	ctc	gcc	ccc	atc	agc	gcc	gtg	gag	gcc	cta	agg	agc	gcc	1152
288	Val	Arg	Ser	Leu	Ala	Pro	Ile	Ser	Ala	Val	Glu	Ala	Leu	Arg	Ser	Ala	
289		370					375					380					
291	gag	gac	ctt	ttg	ttg	cgc	tac	ggg	ggg	cac	aag	gag	gcg	gcg	ggc	ttc	1200
292	Glu	Asp	Leu	Leu	Leu	Arg	Tyr	Gly	Gly	His	Lys	Glu	Ala	Ala	Gly	Phe	
293	385					390					395				400		
295	gcc	atg	gac	gag	gcc	ctc	ttc	ccc	gcc	ttc	aag	gcc	cgg	gtg	gag	gcc	1248
296	Ala	Met	Asp	Glu	Ala	Leu	Phe	Pro	Ala	Phe	Lys	Ala	Arg	Val	Glu	Ala	
297				405					410					415			
299	tac	gcc	gcc	cgc	ttc	ccc	gac	ccc	gtg	cgc	gag	gtg	gcc	ctt	ttg	gac	1296
300	Tyr	Ala	Ala	Arg	Phe	Pro	Asp	Pro	Val	Arg	Glu	Val	Ala	Leu	Leu	Asp	
301			420					425					430				
303	ctg	ctt	ccg	gag	ccc	ggc	ctc	ctc	ccc	cag	gtc	ttc	cgg	gag	ctc	gcc	1344
304	Leu	Leu	Pro	Glu	Pro	Gly	Leu	Leu	Pro	Gln	Val	Phe	Arg	Glu	Leu	Ala	
305			435				440					445					
307	ctt	ttg	gag	ccc	tac	ggc	gag	gga	aac	ccc	gag	ccc	ctc	ttc	ctc	ctc	1392
308	Leu	Leu	Glu	Pro	Tyr	Gly	Glu	Gly	Asn	Pro	Glu	Pro	Leu	Phe	Leu	Leu	
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311	ttc	ggc	gcc	ccg	gag	gag	gcc	cgg	cgc	ctc	ggg	gag	ggc	cgc	cac	ctc	1440
312	Phe	Gly	Ala	Pro	Glu	Glu	Ala	Arg	Arg	Leu	Gly	Glu	Gly	Arg	His	Leu	
313	465				470				475					480			
315	gcc	ttc	cgc	ctg	aag	ggg	gtg	cgg	gtc	ctg	gcc	tgg	aaa	cag	ggg	gac	1488
316	Ala	Phe	Arg	Leu	Lys	Gly	Val	Arg	Val	Leu	Ala	Trp	Lys	Gln	Gly	Asp	
317				485					490					495			
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324	Ala	Trp	Asn	Gly	His	Leu	Ala	Tyr	Glu	Val	Gln	Ala	Val	Asp	Leu	Arg	
325			515					520					525				
327	aag	cca	gag	gcg	ctg	gag	ggc	ggg	atc	gcg	ccc	ttc	gcc	tac	ccc	ctg	1632
328	Lys	Pro	Glu	Ala	Leu	Glu	Gly	Gly	Ile	Ala	Pro	Phe	Ala	Tyr	Pro	Leu	
329		530				535					540						
331	ccc	ctc	ctc	gag	gcc	ctg	gcc	cgg	gcc	cgc	ctg	ggg	gaa	ggg	gtc	tac	1680
332	Pro	Leu	Leu	Glu	Ala	Leu	Ala	Arg	Ala	Arg	Leu	Gly	Glu	Gly	Val	Tyr	
333	545				550				555					560			
335	gtc	ccc	gag	gac	aac	cct	gag	ggg	ctg	gac	tac	gcc	agg	aag	gcg	ggc	1728
336	Val	Pro	Glu	Asp	Asn	Pro	Glu	Gly	Leu	Asp	Tyr	Ala	Arg	Lys	Ala	Gly	

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date